43. (New) A method for forming a catalogued nucleic acid library from an initial organism sample comprised of heterogeneous organisms, said method comprising:

(a) forming a derived organism sample from the initial organism sample, such that proportional representations of the constituents in said derived organism sample are adjusted to advantage by performing in any order, and at least one time, at least one step selected from the group consisting of: (i) subjecting all or a part of said initial organism sample to a method of selection, and (ii) recovering a fraction of said initial organism sample having at least one desired characteristic;

(b) isolating an initial nucleic acid sample from said derived organism sample;

(c) forming a derived nucleic acid library from said initial nucleic acid sample, such that the proportional representations of the constituents in said derived nucleic acid library are adjusted to advantage by performing in any order, and at least one time, at least one step selected from the group consisting of: (i) subjecting all or a part of said initial nucleic acid sample to a period of selection, (ii) recovering a fraction of said initial organism sample having at least one desired characteristic, and (iii) assembling all or a part of said derived nucleic acid sample into a nucleic acid library;

thereby forming a catalogued nucleic acid library from the heterogeneous organisms.

44. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of the initial organism sample according to at least one organism marker such that the derived organism sample is normalized with respect to organisms exhibiting the at least one organism marker.

45. (New) The method of forming a catalogued nucleic acid library according to claim 44 wherein the at least one organism marker is 16S rRNA content or 18S rRNA content of organisms in the derived organism sample.

46. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of said initial organism sample according to at least one organism marker such that the derived organism sample is selectively enriched with respect to organisms exhibiting the at least one organism marker.

1 (cont'd)

47. (New) The method of forming a catalogued nucleic acid library according to claim 46 wherein the organisms in the derived organism sample exhibit increased 16S rRNA content or 18S rRNA content compared to those in the initial organism sample.

48. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of said initial organism sample according to at least two organism markers such that the derived organism sample is normalized with respect to organisms exhibiting the at least two organism markers.

49. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to nucleic acids exhibiting the at least one organism marker.

50. (New) The method of forming a catalogued nucleic acid library according to claim 49 wherein the at least one nucleic acid marker is G+C content of the nucleic acids in the derived nucleic acid library.

51. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (c) comprises resolving heterogeneity of the initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids exhibiting the at least one nucleic acid marker.

52. (New) The method of forming a catalogued nucleic acid library according to claim 51 wherein the at least one nucleic acid marker is G+C content of the nucleic acids in the derived nucleic acid library.

1 (cont'd)

53. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers such that the derived nucleic acid library is advantageously adjusted with respect to nucleic acids exhibiting each of said at least two organism markers.

54. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of the initial organism sample according to at least one organism marker such that the derived organism sample is normalized with respect to organisms exhibiting said at least one organism marker, and also wherein step (c) comprises resolving heterogeneity of the initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to nucleic acids exhibiting the at least one nucleic acid marker.

55. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein the at least one organism marker is 16S rRNA content or 18S rRNA content of organisms in the derived organism sample.

56. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein the at least one nucleic acid marker is G+C content of the nucleic acids in the derived nucleic acid library.

57. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of said initial organism sample according to at least one organism marker such that the derived organism sample is normalized with respect to organisms that exhibit the at least one organism marker, and also wherein step (c) comprises resolving heterogeneity of the initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids that exhibit the at least one nucleic acid marker.

1 (cont'd)

58. (New) The method of forming a catalogued nucleic acid library according to claim 59 wherein the at least one organism marker is 16S rRNA content or 18S rRNA content of organisms in the derived organism sample.

59. (New) The method of forming a catalogued nucleic acid library according to claim 57 wherein the at least one nucleic acid marker is G+C content of the nucleic acids in the derived nucleic acid library.

60. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of said initial organism sample according to at least one organism marker such that the derived organism sample is normalized with respect to organisms exhibiting the at least one organism marker, and also wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers such that the derived nucleic acid library is advantageously adjusted with respect to nucleic acids exhibiting each of said at least two nucleic acid markers.

61. (New) The method of forming a catalogued nucleic acid library according to claim 60 wherein said at least one organism marker is 16S rRNA content or 18S rRNA content of nucleic acids in the derived nucleic acid library.

62. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of said initial organism sample according to at least one organism marker such that the derived organism sample is selectively enriched with respect to organisms exhibiting the at least one organism marker, and also wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to nucleic acids that exhibit the at least one nucleic acid marker.

63 ~~64.~~ (New) The method of forming a catalogued nucleic acid library according to claim 62 wherein the at least one organism marker is 16S rRNA content or 18S rRNA content of organisms in the derived organism sample.

64. ~~65.~~ (New) The method of forming a catalogued nucleic acid library according to claim ~~64~~ 63 wherein the at least one nucleic acid marker is G+C content of nucleic acids in the derived nucleic acid library.

65. ~~66.~~ (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of said initial organism sample according to at least one organism marker such that the derived organism sample is selectively enriched with respect to organisms exhibiting the at least one organism marker, and also wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids that exhibit the at least one nucleic acid marker.

66.
~~67.~~ (New) The method of forming a catalogued nucleic acid library according to claim ~~66~~ 65 wherein the at least one organism marker is 16S rRNA content or 18S rRNA content of organisms in the derived organism sample.

67.
~~68.~~ The method of forming a catalogued nucleic acid library according to claim 68 wherein the at least one nucleic acid marker is G+C content of nucleic acids in the derived nucleic acid library.

68.
~~69.~~ (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of said initial organism sample according to at least one organism marker such that the derived organism sample is selectively enriched with respect to organisms that exhibit the at least one organism marker, and also wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers such that the derived nucleic acid library is advantageously adjusted with respect nucleic acids that exhibit each of said at least two nucleic acid markers.

69.
~~70.~~ (New) The method of forming a catalogued nucleic acid library according to claim 71 wherein the at least one organism marker is 16S rRNA content or 18S rRNA content of nucleic acids in the derived nucleic acid library.

70.
~~71.~~ (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of said initial organism sample according to at least two organism markers such that the derived organism sample is advantageously adjusted with respect to organisms that exhibit each of said at least two organism markers, and also wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to nucleic acids that exhibit that at least one nucleic acid marker.

71.

~~72.~~ (New) The method of forming a catalogued nucleic acid library according to claim ~~71~~ 70 wherein the at least one nucleic acid marker is the G+C content of nucleic acids in the derived nucleic acid library.

72

~~73.~~ (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises resolving heterogeneity of said initial organism sample according to at least two organism markers such that the derived organism sample is advantageously adjusted with respect to organisms exhibiting each of said at least two organism markers, and also wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids that exhibit the at least one nucleic acid marker.

1 (cont'd)

73

~~74.~~ (New) The method of forming a catalogued nucleic acid library according to claim ~~73~~ 72 wherein the at least one nucleic acid marker is G+C content of the nucleic acids in the derived nucleic acid library.

74

~~75.~~ (New) The method of forming a catalogued nucleic acid library according to any of claims 43-~~74~~ 73 wherein step (b) comprises isolating genomic DNA from the derived organism sample, and wherein step (c) comprises forming a genomic DNA library, thereby forming a catalogued genomic DNA library.

75

~~76.~~ (New) The method of forming a nucleic acid DNA library according to any of claims 43-74 wherein step (b) comprises isolating genomic gene cluster DNA from the derived organism sample, and wherein step (c) comprises forming a genomic gene cluster DNA library, thereby forming a catalogued genomic gene cluster DNA library.

74
77. (New) The method of forming a catalogued nucleic acid library according to any of claims 43-74 wherein step (b) comprises isolating RNA from the derived organism sample, and wherein step (c) comprises forming a cDNA library, thereby forming a catalogued cDNA library.

77.
78. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises forming a derived organism sample that consists of essentially only direct environmental organisms, thereby forming a catalogued nucleic acid library from essentially only direct environmental organisms.

1 (cont'd)

78
79. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises forming a derived organism sample that consists of essentially only direct environmental organisms, and wherein step (b) comprises isolating genomic DNA from the derived organism sample, and also wherein step (c) comprises forming a genomic DNA library, thereby forming a catalogued genomic DNA library from essentially only direct environmental organisms.

79.
80. (New) The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) comprises forming a derived organism sample that consists of essentially only direct environmental organisms, and wherein step (b) comprises isolating genomic gene cluster DNA from the derived organism sample, and also wherein step (c) comprises forming a genomic gene cluster DNA library, thereby forming a catalogued genomic gene cluster DNA library from essentially only direct environmental organisms.